

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

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Application Serial Number: 10/591,752
Source: ILWP
Date Processed by STIC: 09/21/2006

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 01/10/06



IFWP

RAW SEQUENCE LISTING

DATE: 09/21/2006

PATENT APPLICATION: US/10/591,752

TIME: 11:36:46

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Output Set: N:\CRF4\09212006\J591752.raw

4 <110> APPLICANT: Nara Institute of Science, Technology, Research Institute of Innovative

5 Technology for the Earth and Kinki University

W--> 6 <120> TITLE OF INVENTION: Transgenic plants

W--> 7 <130> FILE REFERENCE: C01F1576

C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/591,752

C--> 8 <141> CURRENT FILING DATE: 2006-09-01

W--> 8 <160> NUMBER OF SEQ ID: 18

Does Not Comply
Corrected Diskette Needed

Cp8-1, 2, 3, 5, 6, 7, 8

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21 35 40 45

22 Leu Ala Cys Lys Gln Ile Ala Ser Leu Val Gln Arg Ala Gly Ile Ser

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24 Asn Leu Thr Gly Ile Gln Gly Ala Val Asn Ile Gln Gly Glu Asp Gln

25 65 70 75 80

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27 85 90 95

28 Ser Ser Gly Arg Thr Gly Ile Ile Ala Ser Glu Glu Glu Asp Val Pro

29 100 105 110

30 Val Ala Val Glu Glu Ser Tyr Ser Gly Asn Tyr Ile Val Val Phe Asp

31 115 120 125

32 Pro Leu Asp Gly Ser Ser Asn Ile Asp Ala Ala Val Ser Thr Gly Ser

33 130 135 140

34 Ile Phe Gly Ile Tyr Ser Pro Asn Asp Glu Cys Ile Val Asp Ser Asp

35 145 150 155 160

36 His Asp Asp Glu Ser Gln Leu Ser Ala Glu Glu Gln Arg Cys Val Val

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pls do not insert
any response on line
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Handled by
numeric
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447 gtccatttga aaataccaat gaagatccaa atcgaaaagt gaaaaacatt catagttgga 2820
448 ggaatcgta caattctagt tgcagtaatg ttgattattt attcggcggt aaagacattc 2880
449 ggaatttcat ctctgatgac acttttttag ttagtgatag gaatggagag agttattcca 2940
450 tctattttga tattgaaaat catatttttg agattgacaa cgatcattct tttctgagt 3000
451 aactagaaaag ttctttttat agttatcgaa actcgaatta tcggaataat ggatttaggg 3060
452 gcgaagatcc ctactataat tcttacctgt atgatactca atatagttgg aataatcaca 3120
453 ttaatagttg cattgatagt tatcttcagt ctcaaactct tatagatact tccattataa 3180
454 gtggtagtag gaattacggt gacagttaca tttatagggc cgtttggtgt ggtgaaagtc 3240
455 gaaatagtag tgaaaacgag ggttccagta gacgaactcg cacgaagggc agtgatttaa 3300
456 ctataagaga aagttctaag gatctcgacc tgcaggcatg caagcttggc gtaatcatgg 3360
457 tcatagctgt ttctgtgtg aaattgttat ccgctcacia ttccacacaa catacgagcc 3420
458 ggaagcataa agtgtaaagc ctggggtgcc taatgagtga gctaactcac attaattgcg 3480
E--> 459 ttgcgctcac tgcccgcttt ccagtcggga aacctgtcgt gccagctgca ttaatgaatc 3504
460 ggccaacgcg cggggagagg cggtttgctt attgggcgct cttccgcttc ctgcgtcact 3600
461 gactcgctgc gctcggtcgt tcggctgcgg cgagcggtat cagctcactc aaaggcggtg 3660
462 atacggttat ccacagaatc aggggataac gcaggaaaga acatgtgagc aaaaggccag 3720
463 caaaaggcca ggaaccgtaa aaaggccgcg ttgctggcgt ttttccatag gctccgcccc 3780
464 cctgacgagc atcacaaaaa tcgacgctca agtcagaggt ggcgaaaccc gacaggacta 3840
465 taaagatacc aggcgtttcc ccctggaagc tccctcgtgc gctctcctgt tccgaccctg 3900

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Input Set : A:\pto.da.txt

Output Set: N:\CRF4\09212006\J591752.raw

```

466 ccgcttaccg gatacctgtc cgcctttctc ccttcgggaa gcgtggcgct ttctcaatgc 3960
467 tcacgctgta ggtatctcag ttcggtgtag gtcgttcgct ccaagctggg ctgtgtgcac 4020
468 gaaccccccg ttcagcccca ccgctgcgcc ttatccggta actatcgtct tgagtccaac 4080
469 ccggtaaagac acgacttatc gccactggca gcagccactg gtaacaggat tagcagagcg 4140
470 aggtatgtag gcggtgctac agagtctctg aagtgggtggc ctaactacgg ctacactaga 4200
471 aggacagtat ttggtatctg cgctctgctg aagccagtta ccttcggaaa aagagttggt 4260
472 agctcttgat ccggcaaaaca aaccaccgct ggtagcgggtg gtttttttgt ttgcagcag 4320
473 cagattacyc gcagaaaaaa aggatctcaa gaagatcctt tgatcttttc tacggggtct 4380
474 gacgctcagt ggaacgaaaa ctcacgttaa gggattttgg tcatgagatt atcaaaaagg 4440
475 atcttcacct agatcctttt aaattaaaaa tgaagtttta aatcaatcta aagtatatat 4500
476 gagttaaactt ggtctgacag ttaccaatgc ttaatcagtg aggcacctat ctacgcgatc 4560
477 tgtctatttc gttcatccat agttgcctga ctccccgtcg tgtagataac tacgatacgg 4620
478 gagggcttac catctggccc cagtgtcgca atgataccgc gagacccacg ctacccggct 4680
479 ccagatttat cagcaataaa ccagccagcc ggaagggccg agcgcagaag tggctctgca 4740
480 actttatccg cctccatcca gtctattaat tgttgccggg aagctagagt aagtagttcg 4800
481 ccagttaata gtttgcgcaa cgttgttgcc attgctacag gcacgtggt gtcacgctcg 4860
482 tcgtttggtg tggtttcatt cagctccggt tcccaacgat caaggcgagt tacatgatcc 4920
483 cccatgttgt gcaaaaaaag ggttagctcc ttcggtcctc cgatcgttgt cagaagtaag 4980
484 ttggcccgag ggttatcact catggttatg gcagcactgc ataattctct tactgttatg 5040
485 ccatccgtaa gatgcttttc tgtgactggt gagtactcaa ccaagtcatt ctgagaatag 5100
486 tgtatgcccc gaccgagttg ctcttgcccc gcgtcaatac gggataatac cgcgccacat 5160
487 agcagaactt taaaagtgtc catcattgga aaacgttctt cggggcgaaa actctcaagg 5220
488 atcttaccgc tgttgagatc cagttcgatg taaccactc gtgcacccaa ctgatcttca 5280
489 gcacctttta ctttcaccag cgtttctggg tgagcaaaaa caggaaggca aaatgccgca 5340
490 aaaaagggaa taagggcgac acggaaatgt tgaatactca tactcttctt ttttcaatat 5400
491 tattgaagca tttatcaggg ttattgtctc atgagcggat acatatttga atgtatttag 5460
492 aaaaataaac aaataggggt tccgcgcaca tttccccgaa aagtgccacc tgacgtctaa 5520
493 gaaaccatta ttatcatgac attaacctat aaaaataggc gtatcacgag gccctttcgt 5580
494 c 5581

```

495 <210> SEQ ID NO: 15

496 <211> LENGTH: 1434

497 <212> TYPE: DNA

498 <213> ORGANISM: Nicotiana tabacum

499 <223> OTHER INFORMATION: FbCL

500 <400> SEQUENCE: 15

```

501 atgtcaccac aaacagagac taaagcaagt gttggattca aagctggtgt taaagagtac 60
502 aaattgactt attatactcc tgagtaccaa accaaggat actgatataatt ggcagcattc 120
503 cgagtaactc ctcaacctgg agttccacct gaagaagcag gggccgcggt agctgccgaa 180
504 tcttctactg gtacatggac aactgtatgg accgatggac ttaccagcct tgatcgttac 240
505 aaagggcgat gctaccgcat cgagcgtgtt gttggagaaa aagatcaata tattgcttat 300
506 gtagcttacc ctttagacct ttttgaagaa ggttctgtta ccaacatgtt tacttccatt 360
507 gtaggtaacg tatttggtgt caaagccctg cgcgctctac gtctggaaga tctgcgaatc 420
508 cctcctgctt atgttaaaac tttccaaggt ccgcctcatg ggatccaagt tgaaagagat 480
509 aaattgaaca agtatggtcg tcccctgttg ggatgtacta ttaaacctaa attgggggta 540
510 tctgctaaaa actacggtag agccgtttat gaatgtcttc gcggtggact tgattttact 600
511 aaagatgatg agaacgtgaa ctcaacaaca tttatgcgtt ggagagatcg tttcttattt 660
512 tgtgccgaag cactttataa agcacaggct gaaacagggt aaatcaaaagg gcattacttg 720
513 aatgctactg caggtacatg cgaagaaatg atcaaaaagag ctgtatttgc tagagaattg 780
514 ggcgttccga tcgtaatgca tgactactta acggggggat tcaccgcaaa tactagcttg 840

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```

515 gctcattatt gccgagataa tgggtctactt cttcacatcc accgtgcaat gcatgcggtt      900
516 attgatagac agaagaatca tgggtatccac ttccgggtat tagcaaaagc gttacgtatg      960
517 tctgggtggag atcatattca ctctgggtacc gtagtaggta aacttgaagg tgaaagagac    1020
518 ataactttgg gctttgttga tttactgcgt gatgattttg ttgaacaaga tcgaagtcgc      1080
519 ggtatttatt tcaactcaaga ttgggtctct ttaccagggtg ttctaccggt ggcttcaggga    1140
520 ggtattcacg tttggcatat gcctgctctg accgagatct ttggggatga ttccgtacta      1200
521 cagttcggtg gaggaacttt aggacatcgt tggggtaatg cgccagggtg cgtagctaat      1260
522 cgagtagctc tagaagcatg tgtaaaagct cgtaaatgaag gacgtgatct tgctcaggaa      1320
523 ggtaaatgaaa ttattcgca ggcttgcaaa tggagcccgg aactagctgc tgcttgtaga      1380
524 gtatggaaa agatcgtatt taattttgca gcagtggacg ttttggataa gtaa              1434

```

525 <210> SEQ ID NO: 16

526 <211> LENGTH: 705

527 <212> TYPE: DNA

528 <213> ORGANISM: Nicotiana tabacum → <220>

529 <223> OTHER INFORMATION: accD

530 <400> SEQUENCE: 16

```

531 aatgactatt catctattgt attttcatgc aaataggggg caagaaaact ctatggaaaag      60
532 atggtgggtt aattcgatgt tgtttaagaa ggagttcgaa cgcagggtgt ggctaaataa      120
533 atcaatgggc agtcttggtc ctattgaaa atcaaatgaa gatccaaatc gaaaagtga      180
534 aaacattcat agttggagga atcgtgacaa ttctagttgc agtaatgttg attatttatt      240
535 cggcggttaa gacattcgga atttcatctc tgatgacact tttttagtta gtgataggaa      300
536 tggagacagt tattccatct attttgatat tgaaaatcat atttttgaga ttgacaacga      360
537 tcattctttt ctgagtgaac tagaaagttc tttttatagt tatcgaaaact cgaattatcg      420
538 gaataatgga tttaggggag aagatcccta ctataattct tacatgtatg atactcaata      480
539 tagttggaat aatcacatta atagttgcat tgatagttat cttcagttc aaatctgtat      540
540 agatacttcc attataagtg gtagtgagaa ttacgggtgac agttacattt atagggccgt      600
541 ttgtggtggt gaaagtcgaa atagtagtga aaacgagggt tccagtagac gaactcgac      660
542 gaagggcagt gatttaacta taagagaaaag ttctaattgat ctgca              705

```

543 <210> SEQ ID NO: 17

544 <211> LENGTH: 21

545 <212> TYPE: DNA

546 <213> ORGANISM: Artificial sequence → <220>

W--> 547 .

547 <223> OTHER INFORMATION: polylinker

548 <400> SEQUENCE: 17

549 cgcggccgcg ctagcgtcga c 21

551 <210> SEQ ID NO: 18

552 <211> LENGTH: 7

553 <212> TYPE: DNA

554 <213> ORGANISM: Artificial sequence → <220>

W--> 555 .

555 <223> OTHER INFORMATION: Shine-Dalgarno Sequence

E--> 556 <400> SEQUENCE: 18

557 aggaggu 7

E--> 558 ??

E--> 560 ??

E--> 562 ??

E--> 564 ??

E--> 571 1/14

↘ p/s delete

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Input Set : A:\pto.da.txt

Output Set: N:\CRF4\09212006\J591752.raw

L:6 M:283 W: Missing Blank Line separator, <120> field identifier
L:7 M:283 W: Missing Blank Line separator, <130> field identifier
L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:9 M:283 W: Missing Blank Line separator, <210> field identifier
L:13 M:283 W: Missing Blank Line separator, <220> field identifier
L:13 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:15 M:283 W: Missing Blank Line separator, <400> field identifier
L:15 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:14
L:43 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:66 M:283 W: Missing Blank Line separator, <220> field identifier
L:66 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:68 M:283 W: Missing Blank Line separator, <400> field identifier
L:68 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:67
L:91 M:283 W: Missing Blank Line separator, <220> field identifier
L:91 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:93 M:283 W: Missing Blank Line separator, <400> field identifier
L:93 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:92
L:140 M:283 W: Missing Blank Line separator, <220> field identifier
L:140 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:142 M:283 W: Missing Blank Line separator, <400> field identifier
L:142 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:141
L:164 M:283 W: Missing Blank Line separator, <220> field identifier
L:164 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:165 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:167 M:283 W: Missing Blank Line separator, <400> field identifier
L:167 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:166
L:219 M:283 W: Missing Blank Line separator, <220> field identifier
L:219 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:220 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:221 M:283 W: Missing Blank Line separator, <400> field identifier
L:250 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7
L:250 M:283 W: Missing Blank Line separator, <400> field identifier
L:259 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8
L:259 M:283 W: Missing Blank Line separator, <400> field identifier
L:268 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:9
L:268 M:283 W: Missing Blank Line separator, <400> field identifier
L:287 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:288 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:10
L:288 M:283 W: Missing Blank Line separator, <400> field identifier
L:370 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:371 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:11
L:371 M:283 W: Missing Blank Line separator, <400> field identifier
L:378 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:12
L:378 M:283 W: Missing Blank Line separator, <400> field identifier
L:387 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:13
L:387 M:283 W: Missing Blank Line separator, <400> field identifier

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Input Set : A:\pto.da.txt

Output Set: N:\CRF4\09212006\J591752.raw

L:399 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:400 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:14
L:400 M:283 W: Missing Blank Line separator, <400> field identifier
L:459 M:254 E: No. of Bases conflict, LENGTH:Input:3504 Counted:3540 SEQ:14
L:500 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15
L:500 M:283 W: Missing Blank Line separator, <400> field identifier
L:530 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:16
L:530 M:283 W: Missing Blank Line separator, <400> field identifier
L:547 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:548 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:17
L:548 M:283 W: Missing Blank Line separator, <400> field identifier
L:555 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:556 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:18
L:556 M:283 W: Missing Blank Line separator, <400> field identifier
L:558 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:560 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:562 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:562 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:564 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:564 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:571 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18
L:571 M:254 E: No. of Bases conflict, LENGTH:Input:14 Counted:8 SEQ:18
L:571 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:571 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7 Found:8 SEQ:18